

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:12:05 ; Search time 69.2267 Seconds
2810.909 Million cell updates/sec

Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LPHSVCTDVCPFGTGRFTQ.....TVSTVLDRLIIMCPLKIQ 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : UniProt_03;*
1: uniprot_sprot:
2: uniprot_trembl:
* pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1906	96.0	755	2	Q8NGV9		Q8ngv9 homo sapien
2	1749	88.1	365	2	Q8TDU1		Q8tdu1 homo sapien
3	1450	73.0	428	2	070413		070413 rattus norv
4	1444	72.7	912	2	070410		070410 mus musculu
5	904.5	45.5	230	2	070414		070414 rattus norv
6	791.5	39.9	458	2	093555		093555 carassius a
7	787.5	39.7	848	2	093553		093553 carassius a
8	775.5	39.0	362	2	Q9PSY1		Q9psy1 carassius a
9	775.5	39.0	408	2	093558		093558 carassius a
10	769.5	38.7	844	2	093552		093552 carassius a
11	755.5	38.0	350	2	093556		093556 carassius a
12	753.5	37.9	880	2	073639		073639 fugu rubrip
13	751	37.8	875	2	073640		073640 fugu rubrip
14	747	37.6	856	2	073638		073638 fugu rubrip
15	736.5	37.1	1027	2	08J104		Q8j104 squalusaca
16	722	36.4	864	2	073637		073637 fugu rubrip
17	715.5	36.0	783	2	Q8CDP3		Q8cdp3 mus musculu
18	714.5	36.0	1079	1	CASR_MOUSE		Q9qy96 mus musculu
19	714.5	36.0	1079	1	CASR_RAT		P48442 rattus norv
20	713.5	35.9	1079	2	Q80ZA8		Q80za8 rattus norv
21	711.5	35.8	1078	1	CASR_HUMAN		P41180 homo sapien
22	709.5	35.7	1085	1	CASR_BOVIN		P35384 bos taurus
23	702.5	35.4	868	2	073636		073636 fugu rubrip
24	696.5	35.1	854	2	Q6UNX3		Q6unx3 ictalurus p
25	696	35.0	941	2	Q6XAFL		Q6xafl salmo salar
26	696	35.0	941	2	Q6XAF3		Q6xafl3 salmo salar
27	678.5	34.2	940	2	073635		073635 fugu rubrip
28	675	34.0	940	2	Q90WL6		Q90wl6 sparus aura
29	660	33.2	850	2	Q6XAFL2		Q6xafl2 salmo salar
30	644	32.4	157	2	Q99PC0		Q99pc0 rattus norv
31	640.5	32.3	866	2	Q35268		Q35268 rattus norv

ALIGNMENTS

070409	mus musculu	070409	mus musculu
Q6tac4	mus musculu	Q6tac4	mus musculu
Q80Z08	mus musculu	Q80Z08	mus musculu
035272	rattus norv	035272	rattus norv
070411	rattus norv	070411	rattus norv
Q86un7	homo sapien	Q86un7	homo sapien
035192	mus musculu	035192	mus musculu
Q80Z09	mus musculu	Q80Z09	mus musculu
035267	rattus norv	035267	rattus norv
035193	mus musculu	035193	mus musculu
035269	rattus norv	035269	rattus norv
035191	mus musculu	035191	mus musculu
035266	rattus norv	035266	rattus norv
035189	mus musculu	035189	mus musculu

RESULT 2

QY	313	GCIFAPKCLLRLPERNTSEIVCGRVSTTDNCIQLTSASFVSSLENNNTTVSTVLDDRVLI	372	Putative pheromone receptor V2R2 (Fragment).
Db	688	GCIFAPKCLLRLPERNTSEIVCGRVSTTDNCIQLTSASFVSSLENNNTTVSTVLDDRVLI	747	Rattus norvegicus (Rat).
QY	373	YMCPLKLQ	380	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Db	748	YMCPLKLQ	755	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

Q8TDU1 PRELIMINARY; PRT; 365 AA.

ID Q8TDU1; AC Q8TDU1; DT 01-JUN-2002 (TREMBLrel. 21, Created); DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update); DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update); DE Putative G-protein coupled receptor.

GN Name=GPCR; OS Homo sapiens (Human). DR GO: 0008067; F:metabotropic glutamate, GABA-B-like receptor. . . ; IEA. DR GO: 0004872; F:receptor activity; IEA. DR GO: 0004872; G:protein activity; IEA. DR GO: 0004872; InterPro; IPR000337; GPCR Mgr.

RN 1; RN SEQUENCE FROM N.A. DR PFAM; PF00003; 7tm_3; 1. RA Takeda S., Kadowaki S., Takaesu H., Mitaku S.; RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AB083610; BAB89323.1; -. DR GO: 0016020; C:membrane; IEA. DR GO: 0008067; F:metabotropic glutamate, GABA-B-like receptor. . . ; IEA. DR GO: 0004872; F:receptor activity; IEA. DR GO: 0004872; InterPro; IPR000337; GPCR Mgr.

RN 2; RN SEQUENCE FROM N.A. DR PFAM; PF00003; 7tm_3; 1. RA Takeda S., Kadowaki S., Takaesu H., Mitaku S.; RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AB083610; BAB89323.1; -. DR GO: 0016020; C:membrane; IEA. DR GO: 0008067; F:metabotropic glutamate, GABA-B-like receptor. . . ; IEA. DR GO: 0004872; F:receptor activity; IEA. DR GO: 0004872; InterPro; IPR000337; GPCR Mgr.

DR PRINTS; PR00248; GPCRMGR. DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1. DR Receptor.

KW NON_TER 1; SQ SEQUENCE 428 AA; 47708 MW; EFB69A78F750E202 CRC64; Query Match 73.0%; Score 1450; DB 2; Length 428; Best Local Similarity 75.5%; Pred. No. 1.4e-97; Matches 277; Conservative 35; Mismatches 55; Indels 0; Gaps 0;

QY 2 PHSVCTDVCPPGTRGTFQREPICCFDSIPCAADGHVSRKPGERECQCGEDYWNSNAQKSE 61 Db 62 PDSFCTQVCPGPTRKGIRQGPICCFDCIPCAADGYVSENPGQRECDDPGEDDWNSNAEKS 121

QY 62 CVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRRHTPLVYNASPDWLGFLIQVS 121 Db 122 CVPKLVEFLAYEEALGFTLVLSIFGALVVLAUTVTVYVYRHTPLVYKANDRELSELIQMS 181

QY 122 LIMMLSSMLFIDKPNAWSCMAGQVTLALGFSLCLSGKTSLEFLAYRISKTKQLTS 181 Db 182 LVITVLSMLPIGKSCHWTMRCQVTLALGFCLCLSSTLGTKTISLPAYRISKTKRLIS 241

QY 182 MHPLYRKIIIVLISVLAEGICTAAYLILEPPPMVYKNMESQNTKIIILGCNEISIEFLYSMFG 241 Db 242 MSPYRKLIIVLICVVGEIGVCAAYLVLEPPPRMFKNIEPQNVKIIFPECNEGSIPEFLCAIFG 301

QY 97 VYYTHRHTPLVNADWQLGFELIQVSLLIIMLSSMLFIDKPNAWSCMAGQVTLALGFSLCL 156 Db 142 SCLLGKTSSSLFLAYRISKSKTQLTSMHPLYRKIIIVLISVLAEGICTAAYLILEPPMVYKN 201

QY 157 SCLLGKTSSSLFLAYRISKSKTQLTSMHPLYRKIIIVLISVLAEGICTAAYLILEPPMVYKN 216 Db 142 SCLLGKTSSSLFLAYRISKSKTQLTSMHPLYRKIIIVLISVLAEGICTAAYLILEPPMVYKN 201

QY 217 MESQNTKIIILGCNEISIEFLYSMFGIDAFLALLCFLTTFVARQLPDNYYEGKCITFGMLV 276 Db 202 MESQNTKIIILGCNEISIEFLYSMFGIDAFLALLCFLTTFVARQLPDNYYEGKCITFGMLV 261

QY 277 FPIIWMFSFPVYVLSTKGGKFKADEVIAAILASSHGLLGCIFAPKCLLILLRPERNTSEIVC 336 Db 262 FPIIWMFSFPVYVLSTKGGKFKADEVIAAILASSHGLLGCIFAPKCLLILLRPERNTSEIVC 321

QY 337 GRVSTTDNCIQLTSASFVSSLENNNTTVSTVLDDRVLIYMCPLKLQ 380 Db 322 GRVSTTDNCIQLTSASFVSSLENNNTTVSTVLDDRVLIYMCPLKLQ 365

RESULT 3

070413	PRELIMINARY;	PRT;	428 AA.
ID 070413;	AC 070413;	DT 01-AUG-1998 (TREMBLrel. 07, Created)	
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)	DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)		
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DE Putative pheromone receptor V2R2.		
	OS Mus musculus (Mouse).		

RESULT 4

O70410	PRELIMINARY;	PRT;	912 AA.
ID O70410;	AC 070410;	DT 01-AUG-1998 (TREMBLrel. 07, Created)	
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		

DB Putative pheromone receptor V2R2B (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vomeronasal neurons;
 RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
 RA Ryba N.J.; Tirindelli R.;
 RT "A new multigene family of putative pheromone receptors.";
 RL Neuron 19:371-379(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vomeronasal neurons;
 RA Ryba N.J.P.; Tirindelli R.;
 RL Submitted ('MAR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF053986; AAC08413.1;
 DR HSSP; P23385; 1EWK.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; IEA.
 DR DR InterPro; IPR004872; F:receptor activity; IEA.
 DR DR InterPro; IPR001828; ANF receptor.
 DR DR InterPro; IPR000068; Ca⁻sens receptor.
 DR DR InterPro; IPR000337; GPCR_Mgr.
 DR DR InterPro; IPR011500; NCD3G_GPCR.
 DR DR Pfam; PF00003; 7tm_3; 1.
 DR DR Pfam; PF01094; ANF receptor; 1.
 DR DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
 DR DR Receptor.
 FT NON TER
 SQ SEQUENCE 1 1
 DR DR 230 AA; 25703 MW; 274BEF5F4D72F404 CRC64;
 DR DR 45.5%; Score 904.5; DB 2; Length 230;
 DR DR Best Local Similarity 76.6%; Pred. No. 4.1e-58;
 DR DR Matches 177; Conservative 20; Mismatches 33; Indels 1; Gaps 1
 DR DR Query Match 138 NWSCMAGQVTLLALGFSLCLSCLLGKTSSLFLAYRISKSQTQLTSMHPLYRKIIIVLISVLA 197
 DR DR 1 NWTCMARQVTLLALGFCLCLSSILGKTISLPAYRISKSQTLLSMHPIFRKLIVLICVVG 60
 DR DR 61 EIGVCTAYLMLKKPPRMVNQIEPQNVTKIIFBCNEGSSIFELCSIPAFDVLLALLCFLTTFVA 257
 DR DR 198 RQLPDNYYEGKCITFGMLVFPIIIMSFPVVYLSTKGKFQMAVEIFAILASSHGLLGCIFA 317
 DR DR 61 EIGVCTAYLMLKKPPRMVNQIEPQNVTKIIFBCNEGSSIFELCSIPAFDVLLALLCFLTTFVA 120
 DR DR 258 RQLPDNYYEGKCITFGMLVFPIIIMSFPVVYLSTKGKFQMAVEIFAILASSHGLLGCIFA 317
 DR DR 62 CVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYIHRHTPLVNASDWQLGFLIQVS 121
 DR DR 606 CVPKLVEFLAYGEAIDGFTLVILSIFGALVVLAVTYYVIIHRHTPLVKANDRELSFLIQMS 665
 DR DR 122 LIIMLLSSMLFIDKPHNNSCMAGQVTLLALGFSLCLSCLLGKTSSLFLAYRISKSQTQLTS 181
 DR DR 666 LVITVLSLLFIGKPCNWSMCARQITLALGFCLCLSSILGKTISFFAYRISVSKTRLIS 725
 DR DR 182 MHPLYRKIIIVLISVLAEGIGCTAYLILEPPMVVKNMESQNTKIIILGNCNEISIEFLYSMFG 241
 DR DR 726 MPHPIERKLIIVLVCVNGEIGVCAAYVLEPPRMPKNIETQNVKLIIFBCNEGSSVELCSIFG 785
 DR DR 093555 PRELIMINARY; PRT; 458 AA.
 DR DR ID 093555; AC 093555;
 DR DR DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DR DR DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DR DR DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DR DE Putative odorant receptor (Fragment).
 DR GN Name=GFB7;
 DR OS Carassius auratus (Goldfish).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 DR OC Actinopterygi; Neopterygi; Teleostei; Ostariophysii; Cypriniformes;
 DR OC Cyprinidae; Carassius.
 DR RN NCBI_TaxID=7957;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
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 RA Cao Y.; Oh B.C.; Stryer L.;
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 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
 RA Cao Y.; Oh B.C.; Stryer L.;
 RT "Cloning and localization of two multigene receptor families in
 RT Goldfish olfactory epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
 DR EMBL; AF083084; AAC64079.1;
 DR RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=98426265; PubMed=97

RESULT 7

O93553 PRELIMINARY; PRT; 848 AA.

ID O93553; PRELIMINARY; PRT; 848 AA.

AC 093553; PRELIMINARY; PRT; 848 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Putative odorant receptor.

GN Name=GFB8;

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

RA Cao Y., Oh B.C., Stryer L.; "Cloning and localization of two multigene receptor families in goldfish olfactory epithelium." Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).

RT Goldfish olfactory epithelium.

RL EMBL; AF083082; AAC64077.1;

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008067; F:receptor activity; IEA.

DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . . ; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . . ; IEA.

DR InterPro; IPR001828; ANF receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR InterPro; IPR011500; NCD3G_GPCR.

DR InterPro; IPR004073; Vmron_receptor2.

DR Pfam; PF00003; 7tm_3_1.

DR Pfam; PF01094; ANF receptor; 1.

DR Pfam; PF07562; NCD3G_1.

DR PRINTS; PRO0248; GPCRMGR.

DR PRINTS; PR01535; VOMERONASL2R.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.

KW Receptor.

FT NON_TER 1

SQ SEQUENCE 458 AA; 51119 MW; 583EE81671F71697 CRC64;

Query Match 39.9%; Score 791.5; DB 2; Length 458;

Best Local Similarity 42.6%; Pred. No. 1.4e-49;

Matches 145; Conservative 74; Mismatches 120; Indels 1; Gaps 1;

Qy 2 PHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKS 61

Db 115 PRSVCSESCPPGTRKAAQKGRPVCCYDCIPCAEGEISNETDSINCCKQCPGEYWPAEKNR 174

Qy 62 CVLKAVEYLAYDEALGFTLVLSVFGAFVFLAVTAVVVIHRHTPLVYNASDWQLGFLIQVS 121

Db 175 CVLKAVEFLSFTEIMGIVLVFFSLFVGGLTVLVALIFYSKKNTPIVKANNSELSFLILFS 234

Qy 122 LIIMLSSMLFDKPHNSCMAGQVTLALGFLSCLSLGKTSSLPLAYRISKSTQLT 181

Db 235 LSLCFLCSLTFIGRPTEWSCMLRHTAFGITFVLCISCLGKTMVVLMMAFKATLPGSNVMK 294

Qy 182 -MPLIYRKIVLVLISVLABIGCTAYLLEPPMVYKONESQNTKILLGCNEISIEFLYSMF 240

Db 295 WFGPAQQRFVSLAFTLIIQVLICLLWLTISSPPYPHKNNKYKEKIIIECSLRLSTLGFWAVL 354

Qy 241 GIDAFLLALCFLTTFVARQLPDNNYYEGKCITFGMLVFFIIWMSFPVYLSTKGKFKMAVE 300

Db 355 GYVGLLAVLCFLIAFLARTLPDNFNEAKFTFSMLIFCAVWTFIPAYVSSPGKFTVAV 414

Qy 301 IFAILASSHGLLGCIFAPKCLLIRRPERNTSEIYCCGRVS 340

Db 415 IFAILASSHGLLGCIFAPKCYTILLKDQNTKOHVNGKTT 454

RESULT 8

Q9PSY1 PRELIMINARY; PRT; 362 AA.

ID Q9PSY1 PRELIMINARY; PRT; 362 AA.

AC Q9PSY1; PRELIMINARY; PRT; 362 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DB Putative odorant receptor (Fragment).

GN Name=GFB2;

OS Carassius auratus (Goldfish).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

RA Cao Y., Oh B.C., Stryer L.; "Cloning and localization of two multigene receptor families in goldfish olfactory epithelium." Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).

RT Goldfish olfactory epithelium.

RL EMBL; AF083082; AAC64077.1;

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008067; F:receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . . ; IEA.

DR	Pfam; PF07562; NCD3G; 1.
DR	PRINTS; PR00248; GPCR_MGR.
DR	PRINTS; PR01535; VOMERONASL2R.
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW	Receptor.
FT	NON TER 1 1 MW; BFF09201800FC13F CRC64;
SQ	SEQUENCE 362 AA; 40359 MW; 8A61F477475FB24B CRC64;
Query Match	39.0%; Score 775.5; DB 2; Length 408;
Best Local Similarity	42.9%; Pred. No. 1..6e-48;
Matches	146; Conservative 71; Mismatches 122; Indels 1; Gaps 1;
QY	1 LPHSVCTDVCPGTGRGFVQREPICCFDSI PCADGHVSRKGERECEOCGEDIWSNAOKS 60
Db	18 VPVSVCSDSCLPGTRKAVKNGRPVCCYDCINCADGEISNETDSDLDCHECLPEYWPNNKDD 77
QY	61 ECVLKKEVEYLAYDEALGFTLVILSVFGAFVLAUTAVYVIHREHTPLVNADWQLGFELIQV 120
Db	78 KCLPKPVEFSLWDILGIIAFAFSVAGSLVALSITLVPYKNRTSPIVKANNSELSPLLLF 137
QY	121 SIIIMLSSMLFDIKPHNWSMAGQVTLALGPSLCLSCLLGKTSSLFLAYRISKSTQLT 180
Db	138 SLTLSFLCALTFIGRPTEWSCMLRHTAFIGTFLVLCISCVLGKTIIVVLIAKATLPGSNVM 197
QY	181 S-MHPLYRKIIIVLISVLAEIGICTAYLILEPPMVYKNCMESQNTKILGCBNBSIEFLYSM 239
Db	198 KWFGPLQQRLSVLGFITLQVQLICVWLKITYPPFPYNNMHQYKEKITLECSLGSAILGMNAV 257
QY	240 FGIDAFALLCFLTTFVARQLPDNYEGKCITFGMLVFFITWMSFVPVYLSTKGKPKMAV 299
Db	258 LGYIGLLAFLCFVLAFLARKLKDPNFNEAKFITEFSMLIFCAVWITFIPSYVSSSPGKETTVAV 339
QY	300 BIPAILASHGLLGCIFAPKCLILLRPERNTSEIVCGRV 339
Db	318 BIPAILASSFGLLCIFAPKCFIVFRPEQNTKKHLMGKV 357
RESULT 10	093552 PRELIMINARY; PRT; 844 AA.
ID	093552 ID 093552 PRELIMINARY; PRT; 844 AA.
AC	093552 AC 093552 PRELIMINARY; PRT; 844 AA.
DT	01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Putative odorant receptor (Fragment). Name=GFB14;
GN	Carassius auratus (Goldfish).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Cyprinidae; Carassiidae; Carassius.
OX	[1]
RN	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RX	TISSUE=Olfactory epithelium; MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
RA	Cao Y., Oh B.C., Stryer L.; "Cloning and localization of two multigene receptor families in goldfish olfactory epithelium." Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992 (1998).
RT	"Cloning and localization of two multigene receptor families in goldfish olfactory epithelium." DR GO:0016020; C:membrane; IEA. DR GO:0008067; F:metabotropic glutamate, GABA-B-like receptor. . . ; IEA. DR GO:0004872; F:receptor activity; IEA. DR GO:0007216; F:metabotropic glutamate receptor signaling p. . . ; IEA. DR InterPro; IPR001828; ANF receptor. DR InterPro; IPR000345; CytC heme BS. DR InterPro; IPR000337; GPCR_Mgr. DR InterPro; IPR011500; NCD3G_GPCR. DR InterPro; IPR004073; Vmron_receptor2. DR Pfam; PF00003; 7tm_3; 1. DR Pfam; PF01094; ANF receptor; 1. DR Pfam; PF07562; NCD3G; 1.
QY	Query Match 39.0%; Score 775.5; DB 2; Length 408;
Best Local Similarity	42.9%; Pred. No. 1..8e-48;
Matches	146; Conservative 71; Mismatches 122; Indels 1; Gaps 1;
QY	1 LPHSVCTDVCPGTGRGFVQREPICCFDSI PCADGHVSRKGERECEOCGEDIWSNAOKS 60
Db	64 VPVSVCSDSCLPGTRKAVKNGRPVCCYDCINCADGEISNETDSDLDCHECLPEYWPNNKDD 123
QY	61 ECVLKKEVEYLAYDEALGFTLVILSVFGAFVLAUTAVYVIHREHTPLVNADWQLGFELIQV 120
Db	124 KCLPKPVEFSLWDILGIIAFAFSVAGSLVALSITLVPYKNRTSEIVKANNSELSPLLLF 183
QY	121 SIIIMLSSMLFDIKPHNWSMAGQVTLALGPSLCLSCLLGKTSSLFLAYRISKSTQLT 180
Db	184 SLTLSFLCALTFIGRPTEWSCMLRHTAFIGTFLVLCISCVLGKTIIVVLIAKATLPGSNVM 243
QY	181 S-MHPLYRKIIIVLISVLAEIGICTAYLILEPPMVYKNCMESQNTKILGCBNBSIEFLYSM 239
Db	244 KWFGPLQQRLSVLGFITLQVQLICVWLKITYPPFPYNNMHQYKEKITLECSLGSAILGMNAV 303
QY	240 FGIDAFALLCFLTTFVARQLPDNYEGKCITFGMLVFFITWMSFVPVYLSTKGKPKMAV 299
Db	304 LGYIGLLAFLCFVLAFLARKLKDPNFNEAKFITEFSMLIFCAVWITFIPSYVSSSPGKETTVAV 363
QY	300 BIPAILASHGLLGCIFAPKCLILLRPERNTSEIVCGRV 339
Db	364 BIPAILASSFGLLCIFAPKCFIVFRPEQNTKKHLMGKV 403

DR	PRINTS; PRO0248; GPCRMGR.	KW	Receptor.
DR	PROSITE; PR01535; VOMERONASL2R.	FT	NON_TER
DR	PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.	SQ	SEQUENCE
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.	350 AA;	1
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.	39473 MW;	ABE32D19F8729A50 CRC64;
DR	Receptor.	Query Match	38.0%; Score 755.5; DB 2; Length 350;
SQ	SEQUENCE	Best Local Similarity	40.7%; Pred. No. 4.4e-47;
SQ	SEQUENCE	Matches 145; Conservative 71; Mismatches 126; Indels 1; Gaps 1;	Matches 136; Conservative 71; Mismatches 126; Indels 1; Gaps 1;
Qy	2 PHSVCTDVCPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAOKSE 61	Qy	1 LPHSVCTDVCPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAOKS 60
Db	496 PRSACSESCPPGTRKAQKGPRPFCCYDCIPCAEGEIFSNETRFINCKPCPWEYWSNAEKWK 555	Db	12 LPVSVCSEIICPPGTRKAVQKGRPVCYCDCIPCGEGEISNGTDSSDCFCPCDLBYWSNERKD 71
Qy	62 CVLKVEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHPTLVNSDWQLGFLIQVS 121	Qy	61 ECYLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVYIHRHPTLVNSDWQLGFLIQV 120
Db	556 CVLKAVEFLSFTEMGVVLYFVFSLFGVGTLILVAILFYNKDKDTPMVKANNSELSFLILFS 615	Db	72 GCILKVEVEFLYYTBIMGAFCIFSFPTGVLLTAISPLFLYHKETSIVRANNSELSFLILF 131
Qy	122 LIIMLISSMLFIDRPHNWSMCAGQVTTLALGFSLCLSLGKTSSLFLAYRISKSKTQLTS 181	Qy	121 SIIIMLJSSMLFIDKPHNWSMCAGQVTTLALGFSLCLSLGKTSSLFLAYRISKSKTQLT 180
Db	616 LTLCFLCSLTFIGRPTEWSCMLCHTAFGITFVLCISCVLGKTIIVVLMAFKATLPGNNMK 675	Db	132 SLSLCFLCSLTFLGRPTEWSCLMLRPTAFCITVLMMAFKATLPGSNVVM 191
Qy	182 -MHPFLYRKIIVLVLISVLAELIGCTAYLILEPPMVYKOMESQNTKILLGCNEISIEFLYSM 239	Qy	181 S-MHPFLYRKIIVLVLISVLAELIGCTAYLILEPPMVYKOMESQNTKILLGCNEISIEFLYSM 239
Db	676 WFGPAQRQLSVLIAFLTQVTCVWLTLISPPPFPYKQMKYKERIITLECISLGSTIGFWAV 735	Db	192 KWFGPLQQLRSVVSLTFTQIOLIICVWLTLTISPFPYKQMKYKERIITLECNLGSALGFWAV 251
Qy	241 GIDAFLALLCFLTTFVARQLPDNNYYEGKCIITFGMLVFFFIWMSFPVYVLSKTKGKFKMAV 240	Qy	240 FGIDAFLALLCFLTTFVARQLPDNNYYEGKCIITFGMLVFFFIWMSFPVYVLSKTKGKFKMAV 299
Db	736 TYISLIAFLCFLIAFLARTLDPDKFNEAKFTFSMLIFCAVWTFIPAYVSSPGKFTVAVB 795	Db	252 LSYTGLLSVMCFLLAFLARKLPDNFNEAKFTFSMLIFCAVWLTIFIPIAYVSSPGKFTVAV 311
Qy	301 IFAIASSSHGLLGCIFAPKCLLRLPERNTSEIIVCGRVSTTDNC1Q 347	Qy	300 EIFAIASSHGLLGCIFAPKCLLRLPERNTSE 333
Db	796 IFAIASSSSFGLLFGIFAPKCYTLLKPEQNTKQHLIGKTASVSLAQ 842	Db	312 QFAILSSSFGLLFC1FVPKCYTLLRPEKNTKK 345
RESULT 12	PRELIMINARY; PRT; 880 AA.	RESULT 12	PRELIMINARY; PRT; 880 AA.
ID	073639	ID	073639
AC	073639;	AC	073639;
DT	01-AUG-1998 (TREMBLrel. 07, Created)	DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-AUG-1998 (TREMBLrel. 07, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB	Pheromone receptor.	DB	Pheromone receptor.
GN	Name=Ca13;	GN	Name=Ca13;
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bukaryota; Chordata; Craniata; Vertebrata; Euteleostei;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	OC	Actinopterygii; Neopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC	Tetradontoidea; Tetraodontidae; Takifugu.	OC	Tetradontoidea; Tetraodontidae; Takifugu.
NCBI_TaxID	31033;	NCBI_TaxID	31033;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=9826788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;	RX	MEDLINE=9826788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;
RA	Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M., Nakaniishi S., Brenner S.;	RA	Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M., Nakaniishi S., Brenner S.;
RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in Fugu."	RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in Fugu."
RL	Proc. Acad. Sci. U.S.A. 95:5178-5181 (1998).	RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181 (1998).
DR	HSSP; P23385; LEWK.	DR	HSSP; P23385; LEWK.
DR	GO; GO:0016020; C:membrane; IEA.	DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0008067; F:metabotrophic glutamate, GABA-B-like receptor. . . ; IEA.	DR	GO; GO:0008067; F:metabotrophic glutamate, GABA-B-like receptor. . . ; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.	DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0007216; P:metabotrophic glutamate receptor signaling p. . . ; IEA.	DR	GO; GO:0007216; P:metabotrophic glutamate receptor signaling p. . . ; IEA.
DR	InterPro; IPR000337; GPCR Mgr.	DR	InterPro; IPR001828; ANF receptor.
DR	InterPro; IPR011500; NCD3G GPCR.	DR	InterPro; IPR00337; GPCR Mgr.
DR	InterPro; IPR004073; Vmron_receptor2.	DR	InterPro; IPR004073; Vmron_receptor2.
DR	Pfam; PF00003; 7cm_3; 1.	DR	Pfam; PF01094; ANF receptor; 1.
DR	Pfam; PF07562; NCD3G; 1.	DR	Pfam; PF07562; NCD3G; 1.
DR	PRINTS; PRO0248; GPCRMGR.	DR	PRINTS; PRO0248; GPCRMGR.
DR	PRINTS; PRO1535; VOMERONASL2R.	DR	PRINTS; PRO1535; VOMERONASL2R.
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.	DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.	KW	Receptor.

Best Local Similarity Matches 144; Conservative		Pred. No. 4.4e-46;	Mismatches 64; Indels 2; Gaps 2;			Matches 148; Conservative 73; Mismatches 134; Indels 27; Gaps 5;	
Qy	2 PHSYCTDVCPPGTGRGFVQREPIICCFCDSIPCADGHVSRKPGERECEQCGEDYWSNAOKS	61				1 LPHISVCTDVCPPGTGRGFVQREPIICCFCDSIPCADGHVSRKPGERECEQCGEDYWSNAOKS	60
Db	516 PLSVCSQSCIPGFRQAVIKGKPICCFTCVACAAGEEISNSNSAECILQCPLFWSNEDHSQ	575				545 VPFNSNCSDCVPGTRKGIIIEGEPTCCFBCMACAEGEFSDDENDASACTKCPNDFWSNENET	604
Qy	62 CVALKEVEYLAYDEALGFTLVILSVFGAFVFLAVTAVVVIHRHTPLVNASDWQLGFLIQVS	121				61 ECVLKEVEYLAYDEALGFTLVILSVFGAFVFLAVTAVVVIHRHTPLVNASDWQLGFLIQV	120
Db	576 CVPKVIEFLSFEETMGALLAAVSLFGAALTSLVPCVFFRFRHTPLVKASNSELFSFLLF	635				605 SCIAKEIEFLSWTERPFGIALTIFAVLGILLTSFLVGLVFE-AKIPTS--	664
Qy	122 LIIMLSSMLFIDRPHNWSMCAGQVTLLAIGFTLCLSLGGTSSLFLAYRISK-SKTQLT	180				121 SLIIMLSSMLFIDRPHNWSMCAGQVTLLAIGFTLCLSLGGTSSLFLAYRISK-SKTQLT	180
Db	636 LTLCFLCSLTFIGPSRWSCVLRHTAEGITFALCMSCVLAKTAVLFAFTAKRPGNNTVFFY	695				181 SMHPLYRK-----LIVLISVLAELIGICITAYLILEPPMVYKNMESQNTKILLGCNEIS	232
Qy	181 SMHPLYRKIIVLISVLAELIGICITAYLILEPPMVYKNMESQNTKILLGCNEISIEFLYSMF	240				665 SLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCLISCIVLKTNRVLVFE-AKIPTS--	721
Db	696 CSVPLQR-TSVFACITLQVIICVWLTIAPPHPHONTAHAKERIILECNLGSPIWWVTL	754				722 ---LHRKWKVGLNLQFLFLCILQIVTCIWIWLYTAPPSSYRNHELEDEVIFITCDEGS	777
Qy	241 GTDAFLALLCFLTTFVARQLPDNYEGKCITFGMLVFFFIIWMSFVPPVYLSTKGKFXMAVE	300				233 IEFLYSMFGIDAFLALLCFLTTFVARQLPDNYEGKCITFGMLVFFFIIWMSFVPPVYLSTK	292
Db	755 GYIGLLAVICPILAFLARKLPDNFNEAKFTFSMLIFCAVWTFIPAYVSSPGKFTVAWE	814				778 LMALGFLIGYTCLLAACICFFFAFKSRKLPNFNNEAKFTFSMLIFCAVWTFIPAYVSSPGKFTVAWE	837
Qy	301 IFAILASSHGLLGCIFAPKCLLIRRPERNTSEIVCGR 338					293 GKFKMAYEIFFAILASSHGLLGCIFAPKCLLIRRPERNTSEIVCGRVSTTDNCIQLTSAF	352
Db	815 IFAILASSFGLLFCIFAPKCYILIKPEKNTKKHMGR	852				838 GKFKVSAVEVIALASSFGLLGCIFYFNKCYIILFKPCRNTIEEV--RCSTAHAHKVAAARA	895
RESULT 15							
Q8J104	ID Q8J104 PRELIMINARY; PRT; 1027 AA.						
AC	Q8J104; TISSUE=Kidney; MEDLINE=22103704; PubMed=12093923; DOI=10.1073/pnas.152294399; RA Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M., RA Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.; RT "Polyvalent cation receptor proteins (Cars) are salinity sensors in fish." ; RL Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002). DR EMBL; AF406649; AAM7700.1; -.						
RP	SEQUENCE FROM N.A. DR HSSP; P23385; 1 ISS.						
RN	[1]						
RC	DR GO; GO:0016020; C:membrane; IEA: DR GO; GO:0008067; F:metabotropic Glutamate, GABA-B-like receptor. . ; IEA. DR GO; GO:0004872; F:receptor activity; IEA. DR InterPro; IPR001828; ANF receptor. DR InterPro; IPR000668; Ca_sens receptor. DR InterPro; IPR00337; GPCR Mgr. DR InterPro; IPR011500; NCD3G_GPCR. DR Pfam; PF00003; 7tm_3; 1. DR Pfam; PF01094; ANF receptor; 1. DR Pfam; PF07562; NCD3G; 1. DR PRINTS; PR000592; CASENSINGR. DR PRINTS; PR00248; GPCRNGR.						
RA	DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1. DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1. DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1. DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1. KW Receptor. SQ SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;						
RT	Query Match Score 37.1%; Score 736.5; DB 2; Length 1027; Best Local Similarity 38.7%; Pred. No. 3e-45;						